

A-378CIP2C2.ST25.txt
SEQUENCE LISTING



<110> Boyle, William J.
Lacey, David L.
Calzone, Frank J.
Chang, Ming-shi

<120> Osteoprotegerin

<130> A-378CIP2C2

<140> 09/405,032

<141> 1999-09-24

<150> 09/132,985

<151> 1998-08-12

<150> 08/771,777

<151> 1996-12-20

<150> 08/706,945

<151> 1996-09-03

<150> 08/577,788

<151> 1995-12-22

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tcgggctttc ttcttcttct tcttctttcc gcggatcctc gagtaagctt ccatgggtacc 1
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ctgcaggtcg acactagtga gctcgaattc caacgcgtta accatatggt attcctcctt 2
 40

taattagtta aaacaaatct agaatcaaat cgattaatcg actataacaa accattttct 3
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tgcgtaaacc tgtacgatcc tacagggtact tatgttaaac aattgtatct caagcgatat 3
 60

aatagtgtga caaaaatcca atttattaga atcaaagtgc aatctattac cgttttaatg 4
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atatataaca cgcaaaactt gcgacaaaca ataggtaagg ataaagagat gggatatgaaa 4
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gacataaatg ccgacgacac ttacagaata attaataaaa ttaaagcctg tagaagcaat 5
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tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt 13
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actcgaggat ccgcggaaag aagaagaaga agaagaaagc ccgaaaggaa gctgagttgg 14
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<211> 668

<212> DNA

<213> Escherichia coli

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40

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<400> 58

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80

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40

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20

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80

attaaaggag gaataacata tggttaacgc gttggaattc gagctcacta gtgtcgacct 5
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gcagggtacc atggaagctt actcgaggat ccgcggaaag aagaagaaga agaagaaagc 6
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ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa taactagcat aacccttg 6
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48

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<211> 87
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<220>
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60

gctgtgtgat aaatgtgctc cgggtac
87

<210> 72
<211> 81
<212> DNA
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<220>
<223> Synthetic oligonucleotide

<400> 72
ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt
60

ttggaggcag agtttctttc a
81

<210> 73
<211> 71

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 73

gttctcctca tatgaaacat catcaccatc accatcatga aactctgcct ccaaaatacc
60

tgcattacga t

71

<210> 74

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 74

gttctcctca tatgaaagaa actctgcctc caaaatacct gca
43

<210> 75

<211> 76

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 75

tacgcactgg atccttaatg atggtgatgg tgatgatgta agcagcttat tttcacggat
60

tgaacctgat tcccta

76

<210> 76

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 76

gttctcctca tatgaaatac ctgcattacg atccggaaac tggatcat
47

<210> 77

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 77

gttctcctat taatgaaata tcttcattat gatgaagaaa ctt
43

<210> 78

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 78

tacgcactgg atccttataa gcagcttatt tttactgatt
40

<210> 79

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 79

gttctcctca tatggaaact ctgcctccaa aatacctgca
40

<210> 80

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

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tacgcactgg atccttatgt tgcatttcct ttctgaatta gca
43

<210> 81
<211> 18
<212> DNA
<213> Artificial sequence

<220>
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<400> 81
ccggaaacag ataatgag
18

<210> 82
<211> 18
<212> DNA
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<220>
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<400> 82
gatcctcatt atctgttt
18

<210> 83
<211> 30
<212> DNA
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<220>
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<400> 83
ccggaaacag agaagccacg caaaagtaag
30

<210> 84
<211> 30
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<220>

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<400> 84

gacccctact tttgcgtggc ttctctgttt

30

<210> 85

<211> 12

<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

<400> 85

tatgttaatg ag

12

<210> 86

<211> 14

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 86

gacccctcatt aaca

14

<210> 87

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 87

tatgttccgg aaacagttaa g

21

<210> 88

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 88

gacccctaac tgtttccgga aca
23

<210> 89

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 89

tatgttccgg aaacagtgaa tcaactcaaa aataag
36

<210> 90

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 90

gaccccttatt tttgagttga ttcactgttt ccggaaca
38

<210> 91

<211> 100

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 91

ctagcgacga cgacgacaaa gaaactctgc ctccaaaata cctgcattac gatccggaaa
60

ctgggtcatca gctgctgtgt gataaatgtg ctccgggtac
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1

<210> 92

<211> 92
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<220>
<223> Synthetic oligonucleotide

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ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt
60

ttggaggcag agtttctttg tcgtcgtcgt cg
92

<210> 93
<211> 26
<212> DNA
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<220>
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<400> 93
acaaacacaa tcgatttgat actaga
26

<210> 94
<211> 50
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<220>
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<400> 94
tttgttttaa ctaattaaag gaggaataaa atatgagagg atcgcatcac
50

<210> 95
<211> 50
<212> DNA
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<220>
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<400> 95
catcaccatc acgaaacctt cccgccgaaa tacctgcact acgacgaaga

50

<210> 96
<211> 49
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aacctccac cagctgctgt gcgacaaatg cccgccgggt acccaaaca
49

<210> 97
<211> 26
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<220>
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<400> 97
tgtttgggta cccggcgggc atttgt
26

<210> 98
<211> 50
<212> DNA
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<220>
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<400> 98
cgcacagcag ctggtgggag gtttcttcgt cgtagtgcag gtatttcggc
50

<210> 99
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 99

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gggaaggttt cgtgatggtg atggtgatgc gatcctctca tattttatt
49

<210> 100
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 100
cctccttttaa ttagttaaaa caaatctagt atcaaatacga ttgtgtttgt
50

<210> 101
<211> 59
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 101
acaaacacaa tcgatttgat actagatttg ttttaactaa ttaaaggagg aataaaatg
59

<210> 102
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 102
ctaattaaag gaggaataaa atgaaagaaa cttttcctcc aaaatatc
48

<210> 103
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 103

tgtttgggta cccggcggac atttatcaca c
31

<210> 104

<211> 59

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 104

acaaacacaa tcgatttgat actagatttg ttttaactaa ttaaaggagg aataaaatg
59

<210> 105

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 105

ctaattaaag gaggaataaa atgaaaaaaaa aagaaacttt tcctccaaaa tatk
54

<210> 106

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 106

tgtttgggta cccggcggac atttatcaca c
31

<210> 107

<211> 44

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 107
cagcccgggt aaaatggaaa cgtttcctcc aaaatatctt catt
44

<210> 108
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 108
cgtttccatt ttacccgggc tgagcgagag gctcttctgc gtgt
44

<210> 109
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 109
cgctcagccc gggtaaaatg gaaacgttgc ctccaaaata cctgc
45

<210> 110
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 110
ccattttacc cgggctgagc gagaggctct tctgcgtgt
39

<210> 111
<211> 36
<212> DNA
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<220>

<223> Synthetic oligonucleotide

<400> 111

gaaaataagc tgcttagctg cagctgaacc aaaatc
36

<210> 112

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 112

cagctgcagc taagcagctt attttcacgg attg
34

<210> 113

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 113

aaaaataagc tgcttagctg cagctgaacc aaaatc
36

<210> 114

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 114

cagctgcagc taagcagctt atttttactg attgg
35

<210> 115

<211> 102

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 115

ctagaaggag gaataacata tggaaacttt tgctccaaaa tatcttcatt atgatgaaga
60

aactagtcac cagctgctgt gtgataaatg tccgccgggt ac
02

1

<210> 116

<211> 94

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 116

ccggcggaca tttatcacac agcagctgat gactagtttc ttcatacata tgaagatatt
60

ttggagcaaa agtttccata tggtattcct cctt
94

<210> 117

<211> 62

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 117

ctagaaggag gaataacata tggaaacttt tcctgctaaa tatcttcatt atgatgaaga
60

aa

62

<210> 118

<211> 62

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 118
ctagtttctt catcataatg aagatattta gcaggaaaag tttccatatg ttattcctcc
60

tt
62

<210> 119
<211> 51
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 119

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met
1 5 10 15

Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg
20 25 30

Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
35 40 45

Asp Trp His
50

<210> 120
<211> 2432
<212> DNA
<213> Rattus rattus

<220>
<221> CDS
<222> (124)..(1326)
<223>

<400> 120
atcaaaggca gggcatactt cctgttgccc agaccttata taaaacgtca tggttcgcctg
60

ggcagcagag aagcacctag cactggccca gcggctgccg cctgaggttt ccagaggacc
20

1

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aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 68	1
Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile	
1 5 10 15	
att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 16	2
Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr	
20 25 30	
gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 64	2
Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly	
35 40 45	
acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 12	3
Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val	
50 55 60	
cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 60	3
Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu	
65 70 75	
tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 08	4
Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln	
80 85 90 95	
gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 56	4
Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg	
100 105 110	
tac ctg gag ctc gaa ttc tgc ttg aag cac cgg agc tgt ccc cca ggc	5

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04

Tyr Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly

115

120

125

ttg ggt gtg ctg cag gct ggg acc cca gag cga aac acg gtt tgc aaa

5

52

Leu Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys

130

135

140

aga tgt ccg gat ggg ttc ttc tca ggt gag acg tca tcg aaa gca ccc

6

00

Arg Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro

145

150

155

tgt agg aaa cac acc aac tgc agc tca ctt ggc ctc ctg cta att cag

6

48

Cys Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln

160

165

170

175

aaa gga aat gca aca cat gac aat gta tgt tcc gga aac aga gaa gca

6

96

Lys Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala

180

185

190

act caa aat tgt gga ata gat gtc acc ctg tgc gaa gag gca ttc ttc

7

44

Thr Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe

195

200

205

agg ttt gct gtg cct acc aag att ata ccg aat tgg ctg agt gtt ctg

7

92

Arg Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu

210

215

220

gtg gac agt ttg cct ggg acc aaa gtg aat gca gag agt gta gag agg

8

40

Val Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg

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225	230	235	
ata aaa cgg aga cac agc tcg caa gag caa act ttc cag cta ctt aag			8
88			
Ile Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys			
240	245	250	255
ctg tgg aag cat caa aac aga gac cag gaa atg gtg aag aag atc atc			9
36			
Leu Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile			
	260	265	270
caa gac att gac ctc tgt gaa agc agt gtg caa cgg cat atc ggc cac			9
84			
Gln Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His			
	275	280	285
gcg aac ctc acc aca gag cag ctc cgc atc ttg atg gag agc ttg cct			10
32			
Ala Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro			
	290	295	300
ggg aag aag atc agc cca gac gag att gag aga acg aga aag acc tgc			10
80			
Gly Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys			
	305	310	315
aaa ccc agc gag cag ctc ctg aag cta ctg agc ttg tgg agg atc aaa			11
28			
Lys Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys			
320	325	330	335
aat gga gac caa gac acc ttg aag ggc ctg atg tac gca ctc aag cac			11
76			
Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His			
	340	345	350

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ttg aaa gca tac cac ttt ccc aaa acc gtc acc cac agt ctg agg aag 24 Leu Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys	12
355 360 365	
acc atc agg ttc ttg cac agc ttc acc atg tac cga ttg tat cag aaa 72 Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys	12
370 375 380	
ctc ttt cta gaa atg ata ggg aat cag gtt caa tca gtg aag ata agc 20 Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser	13
385 390 395	
tgc tta tagttaggaa tggtcactgg gctgtttctt caggatgggc caacactgat 76 Cys Leu	13
400	
ggagcagatg gctgcttctc cggctcttga aatggcagtt gattcctttc tcatcagttg 36	14
gtgggaatga agatcctcca gcccaacaca cacactgggg agtctgagtc aggagagtga 96	14
ggcaggctat ttgataattg tgcaaagctg ccagggtgtac acctagaaag tcaagcaccc 56	15
tgagaaagag gatattttta taacctcaaa cataggccct ttccttctc tccttatgga 16	16
tgagtactca gaaggcttct actatcttct gtgtcatccc tagatgaagg cctcttttat 76	16
ttattttttt attctttttt tcggagctgg ggaccgaacc cagggccttg cgcttgcgag 36	17
gcaagtgctc taccactgag ctaaattctcc aaccctgaa ggctctttc tttctgcctc 96	17

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tgatagtcta tgacattcct ttttctacaa ttcgtatcag gtgcacgagc cttatcccat 18
56

ttgtaggttt ctaggcaagt tgaccgtag ctatttttcc ctctgaagat ttgattcgag 19
16

ttgcagactt ggctagacaa gcaggggtag gttatgtag tttatttaac agactgccac 19
76

caggagtcca gtgtttcttg ttcctctgta gttgtaccta agctgactcc aagtacattt 20
36

agtatgaaaa ataatcaaca aattttattc cttctatcaa cattggctag ctttggttca 20
96

gggcactaaa agaaactact atatggagaa agaattgata ttgcccccaa cgttcaacaa 21
56

cccaatagtt tatccagctg tcatgcctgg ttcagtgtct actgactatg cgccctctta 22
16

ttactgcatg cagtaattca actggaaata gtaataataa taatagaaat aaaatctaga 22
76

ctccattgga tctctctgaa tatgggaata tctaacttaa gaagctttga gatttcagtt 23
36

gtgttaaagg cttttattaa aaagctgatg ctcttctgta aaagttacta atatatctgt 23
96

aagactatta cagtattgct atttatatcc atccag 24
32

<210> 121
<211> 401
<212> PRT
<213> Rattus rattus

<400> 121

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

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Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60
 Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80
 Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
 85 90 95
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110
 Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
 115 120 125
 Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160
 Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
 165 170 175
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190
 Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205
 Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210 215 220
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu

245

250

255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
 260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
 275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
 290 295 300

Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
 305 310 315 320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
 340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
 370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 385 390 395 400

Leu

<210> 122
 <211> 1324
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (90)..(1292)

<223>

<400> 122

ccttatataa acgtcatgat tgcctgggct gcagagacgc acctagcact gacccagcgg
60

ctgcctcctg aggtttcccg aggaccaca atg aac aag tgg ctg tgc tgc gca 1
13

Met Asn Lys Trp Leu Cys Cys Ala

1

5

ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 1
61

Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu

10

15

20

cct cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 2
09

Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu

25

30

35

40

tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 2
57

Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val

45

50

55

agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 3
05

Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp

60

65

70

agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 3
53

Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys

75

80

85

gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 4
01

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Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val

90

95

100

tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag
49
Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys

105

110

115

120

cac cgg agc tgt ccc ccg ggc tcc ggc gtg gtg caa gct gga acc cca
97
His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala Gly Thr Pro

125

130

135

gag cga aac aca gtt tgc aaa aaa tgt cca gat ggg ttc ttc tca ggt
45
Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe Phe Ser Gly

140

145

150

gag act tca tcg aaa gca ccc tgt ata aaa cac acg aac tgc agc aca
93
Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn Cys Ser Thr

155

160

165

ttt ggc ctc ctg cta att cag aaa gga aat gca aca cat gac aac gtg
41
Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His Asp Asn Val

170

175

180

tgt tcc gga aac aga gaa gcc acg caa aag tgt gga ata gat gtc acc
89
Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile Asp Val Thr

185

190

195

200

ctg tgt gaa gag gcc ttc ttc agg ttt gct gtt cct acc aag att ata
37
Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Ile Ile

205

210

215

cca aat tgg ctg agt gtt ttg gtg gac agt ttg cct ggg acc aaa gtg 7
85

Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly Thr Lys Val

220

225

230

aat gcc gag agt gta gag agg ata aaa cgg aga cac agc tca caa gag 8
33

Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser Ser Gln Glu

235

240

245

caa acc ttc cag ctg ctg aag ctg tgg aaa cat caa aac aga gac cag 8
81

Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Arg Asp Gln

250

255

260

gaa atg gtg aag aag atc atc caa gac att gac ctc tgt gaa agc agc 9
29

Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Ser Ser

265

270

275

280

gtg cag cgg cat ctc ggc cac tcg aac ctc acc aca gag cag ctt ctt 9
77

Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu Gln Leu Leu

285

290

295

gcc ttg atg gag agc ctg cct ggg aag aag atc agc cca gaa gag att 10
25

Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro Glu Glu Ile

300

305

310

gag aga acg aga aag acc tgc aaa tcg agc gag cag ctc ctg aag cta 10
73

Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu Leu Lys Leu

315

320

325

A-378CIP2C2.ST25.txt

ctc agt tta tgg agg atc aaa aat ggt gac caa gac acc ttg aag ggc 11
21
Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly

330

335

340

ctg atg tat gcc ctc aag cac ttg aaa aca tcc cac ttt ccc aaa act 11
69
Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe Pro Lys Thr

345

350

355

360

gtc acc cac agt ctg agg aag acc atg agg ttc ctg cac agc ttc aca 12
17
Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His Ser Phe Thr

365

370

375

atg tac aga ctg tat cag aag ctc ttt tta gaa atg ata ggg aat cag 12
65
Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln

380

385

390

gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg 13
12
Val Gln Ser Val Lys Ile Ser Cys Leu

395

400

gctgtttctt ca 13
24

<210> 123
<211> 401
<212> PRT
<213> Mus musculus

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile
1 5 10 15

A-378CIP2C2.ST25.txt

Glu	Trp	Thr	Thr	Gln	Glu	Thr	Leu	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
			20					25					30			
Pro	Glu	Thr	Gly	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Ala	Pro	Gly	Thr	
		35				40						45				
Tyr	Leu	Lys	Gln	His	Cys	Thr	Val	Arg	Arg	Lys	Thr	Leu	Cys	Val	Pro	
	50					55					60					
Cys	Pro	Asp	His	Ser	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
65					70					75					80	
Val	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Ser	Val	Lys	Gln	Glu	
				85					90					95		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Glu	Glu	Gly	Arg	Tyr	
			100					105					110			
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Ser	
		115					120					125				
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys	
	130					135					140					
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
145					150					155					160	
Ile	Lys	His	Thr	Asn	Cys	Ser	Thr	Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	
				165					170					175		
Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	
			180					185					190			
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
		195					200					205				
Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
	210					215					220					

A-378CIP2C2.ST25.txt

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser
275 280 285

Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305 310 315 320

Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
340 345 350

Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365

Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 124
<211> 1355

A-378CIP2C2.ST25.txt

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (94)..(1296)
<223>

<400> 124
gtatatataa cgtgatgagc gtacgggtgc ggagacgcac cggagcgctc gcccagccgc
60

gcgtccaagc ccctgaggtt tccggggacc aca atg aac aag ttg ctg tgc tgc 1
14
Met Asn Lys Leu Leu Cys Cys
1 5

gcg ctc gtg ttt ctg gac atc tcc att aag tgg acc acc cag gaa acg 1
62
Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr
10 15 20

ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct cat cag ctg 2
10
Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu
25 30 35

ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa cac tgt aca 2
58
Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr
40 45 50 55

gca aag tgg aag acc gtg tgc gcc cct tgc cct gac cac tac tac aca 3
06
Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr
60 65 70

gac agc tgg cac acc agt gac gag tgt cta tac tgc agc ccc gtg tgc 3
54
Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys

A-378CIP2C2.ST25.txt

75	80	85	
aag gag ctg cag tac gtc aag cag gag tgc aat cgc acc cac aac cgc			4
02			
Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg			
90	95	100	
gtg tgc gaa tgc aag gaa ggg cgc tac ctt gag ata gag ttc tgc ttg			4
50			
Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu			
105	110	115	
aaa cat agg agc tgc cct cct gga ttt gga gtg gtg caa gct gga acc			4
98			
Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr			
120	125	130	135
cca gag cga aat aca gtt tgc aaa aga tgt cca gat ggg ttc ttc tca			5
46			
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser			
140	145	150	
aat gag acg tca tct aaa gca ccc tgt aga aaa cac aca aat tgc agt			5
94			
Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser			
155	160	165	
gtc ttt ggt ctc ctg cta act cag aaa gga aat gca aca cac gac aac			6
42			
Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn			
170	175	180	
ata tgt tcc gga aac agt gaa tca act caa aaa tgt gga ata gat gtt			6
90			
Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val			
185	190	195	

A-378CIP2C2.ST25.txt

acc ctg tgt gag gag gca ttc ttc agg ttt gct gtt cct aca aag ttt 38																			7
Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe																			
200					205									210					215
acg cct aac tgg ctt agt gtc ttg gta gac aat ttg cct ggc acc aaa 86																			7
Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys																			
					220									225					230
gta aac gca gag agt gta gag agg ata aaa cgg caa cac agc tca caa 34																			8
Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln																			
					235									240					245
gaa cag act ttc cag ctg ctg aag tta tgg aaa cat caa aac aaa gcc 82																			8
Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala																			
					250									255					260
caa gat ata gtc aag aag atc atc caa gat att gac ctc tgt gaa aac 30																			9
Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn																			
					265									270					275
agc gtg cag cgg cac att gga cat gct aac ctc acc ttc gag cag ctt 78																			9
Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu																			
280					285									290					295
cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga gca gaa gac 26																			10
Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp																			
					300									305					310

A-378CIP2C2.ST25.txt

att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag atc ctg aag 10
74

Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys

315

320

325

ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac acc ttg aag 11
22

Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys

330

335

340

ggc cta atg cac gca cta aag cac tca aag acg tac cac ttt ccc aaa 11
70

Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys

345

350

355

act gtc act cag agt cta aag aag acc atc agg ttc ctt cac agc ttc 12
18

Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe

360

365

370

375

aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg ata ggt aac 12
66

Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn

380

385

390

cag gtc caa tca gta aaa ata agc tgc tta taactggaaa tggccattga 13
16

Gln Val Gln Ser Val Lys Ile Ser Cys Leu

395

400

gctgtttcct cacaattggc gagatcccat ggatgataa 13
55

<210> 125

<211> 401

<212> PRT

<213> Homo sapiens

<400> 125

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg

Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
210						215					220				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
225					230					235					240
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
				245					250					255	
Trp	Lys	His	Gln	Asn	Lys	Ala	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
			260					265					270		
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala
		275					280					285			
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly
	290					295					300				
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys
305					310					315					320
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn
				325					330					335	
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser
			340					345					350		
Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr
		355					360					365			
Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu
	370					375					380				
Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys
385					390					395					400

A-378CIP2C2.ST25.txt

Leu

<210> 126
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 126

Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys
1				5					10					15	

Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro
			20					25					30		

Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala
		35					40					45			

Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys
	50					55					60				

Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr
65					70					75					80

Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn
				85					90					95	

Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His
			100					105					110		

Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly
		115					120					125			

Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys
	130					135				

<210> 127
 <211> 48
 <212> DNA
 <213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 127

ccggcggaca tttatcacac agcagctgat gagaagtttc ttcattcca
48

<210> 128

<211> 219

<212> PRT

<213> Homo sapiens

<400> 128

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	Ala
1				5					10					15	

Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile	Asn	Ser
			20					25					30		

Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	Thr	Gln	Asn
		35					40					45			

Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro	Cys	Pro
	50					55					60				

Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly	Asp	Glu	Pro
65					70					75				80	

Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	Asp	Lys	Ala	His
				85					90					95	

Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	Asp	Glu	Gly	His	Gly
			100					105					110		

Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg
		115					120					125			

Cys	Lys	Pro	Asn	Phe	Phe	Cys	Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp
	130					135					140				

A-378CIP2C2.ST25.txt

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
210 215

<210> 129
<211> 280
<212> PRT
<213> Homo sapiens

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95

A-378CIP2C2.ST25.txt

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr
275 280

<210> 130

<211> 207

<212> PRT

<213> Shope fibroma virus

<400> 130

Met	Leu	Arg	Leu	Ile	Ala	Leu	Leu	Val	Cys	Val	Val	Tyr	Val	Tyr	Gly
1				5					10					15	

Asp	Asp	Val	Pro	Tyr	Ser	Ser	Asn	Gln	Gly	Lys	Cys	Gly	Gly	His	Asp
			20					25					30		

Tyr	Glu	Lys	Asp	Gly	Leu	Cys	Cys	Ala	Ser	Cys	His	Pro	Gly	Phe	Tyr
		35					40					45			

Ala	Ser	Arg	Leu	Cys	Gly	Pro	Gly	Ser	Asn	Thr	Val	Cys	Ser	Pro	Cys
	50					55					60				

Glu	Asp	Gly	Thr	Phe	Thr	Ala	Ser	Thr	Asn	His	Ala	Pro	Ala	Cys	Val
65					70					75					80

Ser	Cys	Arg	Gly	Pro	Cys	Thr	Gly	His	Leu	Ser	Glu	Ser	Gln	Pro	Cys
				85					90					95	

Asp	Arg	Thr	His	Asp	Arg	Val	Cys	Asn	Cys	Ser	Thr	Gly	Asn	Tyr	Cys
			100					105					110		

Leu	Leu	Lys	Gly	Gln	Asn	Gly	Cys	Arg	Ile	Cys	Ala	Pro	Gln	Thr	Lys
		115					120					125			

Cys	Pro	Ala	Gly	Tyr	Gly	Val	Ser	Gly	His	Thr	Arg	Ala	Gly	Asp	Thr
	130					135					140				

Leu	Cys	Glu	Lys	Cys	Pro	Pro	His	Thr	Tyr	Ser	Asp	Ser	Leu	Ser	Pro
145					150					155					160

Thr	Glu	Arg	Cys	Gly	Thr	Ser	Phe	Asn	Tyr	Ile	Ser	Val	Gly	Phe	Asn
				165					170					175	

Leu	Tyr	Pro	Val	Asn	Glu	Thr	Ser	Cys	Thr	Thr	Thr	Ala	Gly	His	Asn
			180					185					190		

A-378CIP2C2.ST25.txt

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr
 195 200 205

<210> 131
 <211> 227
 <212> PRT
 <213> Homo sapiens

<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

A-378CIP2C2.ST25.txt

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220

Gln His Thr
225

<210> 132
<211> 197
<212> PRT
<213> Mus musculus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
85 90 95

A-378CIP2C2.ST25.txt

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
180 185 190

Arg Ala Leu Leu Val
195

<210> 133
<211> 208
<212> PRT
<213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

A-378CIP2C2.ST25.txt

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

<210> 134

<211> 224

<212> PRT

<213> Homo sapiens

<400> 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
20 25 30

A-378CIP2C2.ST25.txt

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

<210> 135

A-378CIP2C2.ST25.txt

<211> 205
 <212> PRT
 <213> Rattus rattus

<400> 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu
 1 5 10 15

Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
 20 25 30

Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
 35 40 45

Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
 50 55 60

Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
 65 70 75 80

Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
 85 90 95

Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
 100 105 110

Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
 115 120 125

His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
 130 135 140

Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp
 145 150 155 160

Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr
 165 170 175

Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp

180

185

190

Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
 195 200 205

<210> 136

<211> 191

<212> PRT

<213> Mus musculus

<400> 136

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
 1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
 20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
 35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
 50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
 65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
 85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
 100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
 115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
 130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro

A-378CIP2C2.ST25.txt

Asn	Arg	Val	Cys	Glu	Cys	Glu	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	
				85					90					95		
Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Ser	Gly	Val	Val	Gln	Ala	
			100					105					110			
Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys	Cys	Pro	Asp	Gly	Phe	
		115					120					125				
Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Ile	Lys	His	Thr	Asn	
	130					135					140					
Cys	Ser	Thr	Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	Gly	Asn	Ala	Thr	His	
145					150					155					160	
Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	Gln	Lys	Cys	Gly	Ile	
				165					170					175		
Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	
			180					185					190			
Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Ser	Leu	Pro	Gly	
		195					200					205				
Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Arg	His	Ser	
	210					215					220					
Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	
225					230					235					240	
Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	
				245					250					255		
Glu	Ser	Ser	Val	Gln	Arg	His	Leu	Gly	His	Ser	Asn	Leu	Thr	Thr	Glu	
			260					265					270			
Gln	Leu	Leu	Ala	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Ile	Ser	Pro	
		275					280					285				

A-378CIP2C2.ST25.txt

Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu
290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
305 310 315 320

Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe
325 330 335

Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His
340 345 350

Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
370 375 380

<210> 139
<211> 380
<212> PRT
<213> Homo sapiens

<400> 139

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
1 5 10 15

Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
20 25 30

Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
65 70 75 80

A-378CIP2C2.ST25.txt

Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	
				85					90					95		
Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	
			100					105					110			
Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	
		115					120					125				
Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	
	130					135					140					
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	
145					150					155					160	
Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	
			165						170					175		
Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	
			180					185					190			
Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	
		195					200					205				
Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	
	210					215					220					
Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	
225					230					235					240	
Lys	Ala	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	
				245					250					255		
Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	
			260					265					270			
Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	
		275					280					285				

A-378CIP2C2.ST25.txt

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile
 290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
 305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe
 325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His
 340 345 350

Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
 355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 370 375 380

<210> 140
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 140
 tggaccaccc agaagtacct tcattatgac
 30

<210> 141
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 141
 gtcataatga aggtacttct ggggtggtcca
 30

<210> 142
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 142
ggaccacca gcttcattat gacgaagaaa c
31

<210> 143
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 143
gtttcttcgt cataatgaag ctgggtgggc c
31

<210> 144
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 144
gtggaccacc caggacgaag aaacctctc
29

<210> 145
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 145
gagaggtttc ttcgtcctgg gtggtccac
29

<210> 146
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 146
cgtttcctcc aaagttcctt cattatgac
29

<210> 147
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 147
gtcataatga aggaactttg gaggaaacg
29

<210> 148
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 148
ggaaacgttt cctgcaaagt accttcatta tg
32

<210> 149
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 149
cataatgaag gtactttgca ggaaacgttt cc

32

<210> 150
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 150
cacgcaaaag tcgggaatag atgtcac
27

<210> 151
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 151
gtgacatcta ttcccgactt ttgcgtg
27

<210> 152
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 152
caccctgtcg gaagaggcct tcttc
25

<210> 153
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 153

gaagaaggcc tcttccgaca ggggtg
25

<210> 154
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 154
tgacctctcg gaaagcagcg tgca
24

<210> 155
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 155
tgcacgctgc tttccgagag gtca
24

<210> 156
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 156
cctcgaaatc gagcgagcag ctcc
24

<210> 157
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 157
cgatttcgag gtctttctcg ttctc
25

<210> 158
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 158
ccgtgaaaat aagctcgta taactaggaa tgg
33

<210> 159
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 159
ccattcctag ttataacgag cttattttca cgg
33

<210> 160
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 160
cctctgagct caagcttccg aggaccacaa tgaacaag
38

<210> 161
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 161
cctctctcga gtcaggtgac atctattcca cacttttgcg tggc
44

<210> 162
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 162
cctctgagct caagcttccg aggaccacaa tgaacaag
38

<210> 163
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 163
cctctctcga gtcaaggaac agcaaacctg aagaaggc
38

<210> 164
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 164
cctctgagct caagcttccg aggaccacaa tgaacaag
38

<210> 165
<211> 38
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 165

cctctctcga gtcactctgt ggtgaggttc gagtggcc
38

<210> 166

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 166

cctctgagct caagcttccg aggaccacaa tgaacaag
38

<210> 167

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 167

cctctctcga gtcaggatgt tttcaagtgc ttgagggc
38

<210> 168

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 168

Met	Lys	His	His	His	His	His	His	His	Ala	Ser	Val	Asn	Ala	Leu	Glu
1				5					10					15	

<210> 169

<211> 70

<212> PRT

<213> Rattus rattus

<400> 169

Ala	Leu	Leu	Val	Phe	Leu	Asp	Ile	Ile	Glu	Trp	Thr	Thr	Gln	Glu	Thr
1				5					10					15	

Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Pro	Glu	Thr	Gly	Arg	Gln	Leu
			20					25					30		

Leu	Cys	Asp	Lys	Cys	Ala	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr
		35					40					45			

Val	Arg	Arg	Lys	Thr	Leu	Cys	Val	Pro	Cys	Pro	Asp	Tyr	Ser	Tyr	Thr
	50					55					60				

Asp	Ser	Trp	His	Thr	Ser
65					70

<210> 170

<211> 120

<212> PRT

<213> Homo sapiens

<400> 170

His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro
1				5					10					15	

Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met
			20					25					30		

Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	Thr
		35					40					45			

Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr
	50					55					60				

Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys
65					70					75					80

Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu
 100 105 110

Gly Cys Arg Leu Cys Ala Pro Leu
 115 120

<210> 171
 <211> 48
 <212> PRT
 <213> Rattus rattus

<400> 171

Tyr Leu His Tyr Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys
 1 5 10 15

Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys
 20 25 30

Thr Leu Cys Val Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His
 35 40 45

<210> 172
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 172

Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu
 1 5 10 15

Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala
 20 25 30

Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp
 35 40 45

Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys
 50 55 60

A-378CIP2C2.ST25.txt

Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val
65 70 75 80

Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
85 90 95

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro
100 105 110

Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn
115 120 125

Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His
130 135